WE CLAIM:

1. A method of detecting the presence of at least one tumor marker mRNA in a sample comprising:

i) providing a sample of cells for analysis;

ii) treating the sample with an oligonucleotide that targets the tumor marker mRNA, wherein the oligonucleotide comprises at least one linked energy donor moiety and at least one linked energy acceptor moiety, wherein said oligonucleotide forms a stem-loop hairpin and wherein said donor and acceptor moieties are separated by at least a portion of a probing nucleobase sequence;

iii) detecting, identifying or quantitating the hybridization of the target sequence under suitable hybridization conditions, wherein the presence, absence or amount of target sequence present in the sample is correlated with a change in detectable signal associated with at least one donor or acceptor moiety of the oligonucleotide; and

iv) detecting, identifying or quantitating the presence of a tumor marker based upon the presence, absence or amount of the hybridization of the oligonucleotide to the target sequence that is determined.

2. The method of claim 1, wherein the tumor marker is one or more of the markers selected from the group consisting of survivin, cyclin D1, Her2/neu, a mutant K-*ras*, chymotrypsinogen, basic fiborblast growth factor, carcinoembryonic antigen, prostate, specific antigen, alpha-fetalprotein, beta-2-microglobulin, bladder tumor antigen, chromogranin A, neuron-specific enolase, S-100, TA-90, tissue polypeptide antigen and human chorionic gonadotropin

3. The method of claim 1, wherein the sample taken from at least one source selected from the group consisting of blood, urine, pancreatic juice, ascites, breast ductal lavage, nipple aspiration, needle biopsy or tissue.

4. The method of claim 3, wherein the tissue is a biopsy from the pancreas or breast.

5. The method of claim 3, wherein the tissue is a frozen section.

6. The method of claim 1, wherein the sample is taken from a breast ductal lavage.

7. The method of claim 1, wherein the sample is taken from pancreatic juice.

8. The method of claim 1, wherein the quantification of the presence of the tumor marker is accomplished by FACS-scan analysis.

9. The method of claim 1, wherein the oligonucleotide is one or more selected from the group consisting of SEQ ID NOS:1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 and 13.

10. The method of claim 1, wherein the oligonucleotide targets the tumor marker survivin.

11. The method of claim 10, wherein the oligonucleotide is one or more selected from the group consisting of SEQ ID NOS: 1, 2 and 9.

12. The method of claim 1, wherein the oligonucleotide targets the tumor marker cyclin D1.

13. The method of claim 12, wherein the oligonucleotide is one or more selected from the group consisting of SEQ ID NOS: 3 and 4.

14. The method of claim 1, wherein the oligonucleotide targets the tumor marker Her2/neu.

15. The method of claim 14, wherein the oligonucleotide is one or more selected from the group consisting of SEQ ID NOS: 5 and 6.

16. The method of claim 1, wherein the oligonucleotide targets the tumor marker a K-*ras* mutant gene.

17. The method of claim 16, wherein the oligonucleotide is one or more selected from the group consisting of SEQ ID NOS: 7, 8, 11, 12 and 13.

18. A method of detecting the presence of a mutant gene in a tumor cell comprising:

i) providing a sample of tumor cells for analysis;

ii) treating the sample with an oligonucleotide that targets the mutant gene, wherein the oligonucleotide comprises at least one linked energy donor moiety and at least one linked energy acceptor moiety, wherein said oligonucleotide forms a stem-loop hairpin and wherein said donor and acceptor moieties are separated by at least a portion of a probing nucleobase sequence;

iii) detecting, identifying or quantitating the hybridization of the oligonucleotide to the mutant gene target sequence under suitable hybridization conditions, wherein the presence, absence or amount of mutant gene target sequence present in the sample is correlated with a change in detectable signal associated with at least one donor or acceptor moiety of the oligonucleotide; and

iv) detecting, identifying or quantitating the presence of a mutant gene based upon the presence, absence or amount of the hybridization of the oligonucleotide to the mutant gene target sequence that is determined.

19. The method of claim 18, wherein the mutant gene is a mutant K-*ras* gene.

20. The method of claim 19, wherein the quantification of the presence of the mutant gene is accomplished by FACS-scan analysis.

21. The method of claim 19, wherein the oligonucleotide is one or more selected from the group consisting of SEQ ID NOS: 7, 8, 11, 12, and 13.

22. A method of monitoring alterations in gene expression in viable cells comprising:

i) providing a sample of viable cells for analysis;

ii) treating the sample with an oligonucleotide that targets a particular gene sequence, wherein the oligonucleotide comprises at least one linked energy donor moiety and at least one linked energy acceptor moiety, wherein said oligonucleotide forms a stem-loop hairpin and wherein said donor and acceptor moieties are separated by at least a portion of a probing nucleobase sequence;

iii) detecting, identifying or quantitating the hybridization of the target sequence under suitable hybridization conditions, wherein the presence, absence or amount of target sequence present in the sample is correlated with a change in detectable signal associated with at least one donor or acceptor moiety of the oligonucleotide; and

iv) detecting, identifying or quantitating the alteration in the expression of the particular gene based upon the presence, absence or amount of the hybridization of the oligonucleotide to the target sequence that is determined.

23. The method of claim 22, wherein the quantification of the alteration in gene expression is accomplished by FACScan analysis and by a fluorescence microplate reader.

24. A method of detecting or monitoring presence or progression of breast cancer in a subject comprising:

i) providing a sample of cells from said subject for analysis;

ii) treating the sample with an oligonucleotide that targets a breast cancer marker gene sequence, wherein the oligonucleotide comprises at least one linked energy donor moiety and at least one linked energy acceptor moiety, wherein said oligonucleotide forms a stem-loop hairpin and wherein said donor and acceptor moieties are separated by at least a portion of a probing nucleobase sequence;

iii) detecting, identifying or quantitating the hybridization of the target oligonucleotide sequence to the breast cancer marker gene sequence under suitable hybridization conditions, wherein the presence, absence or amount of target oligonucleotide sequence present in the sample is correlated with a change in detectable signal associated with at least one donor or acceptor moiety of the oligonucleotide; and

iv) detecting, identifying or quantitating the presence or progression of breast cancer based upon the presence, absence or amount of the hybridization of the oligonucleotide to the breast cancer target sequence that is determined.

25. The method of claim 24, wherein the breast cancer marker is one or more of the markers selected from the group consisting of survivin, cyclin D1, Her2/neu, basic fiborblast growth factor, EGF receptor and carcinoembryonic antigen.

26. The method of claim 24, wherein the sample is taken from at least one source selected from the group consisting of blood, urine, breast ductal lavage, ascites, nipple aspiration, needle biopsy or tissue.

27. The method of claim 26, wherein the tissue is a biopsy from a breast or lymph node.

28. The method of claim 26, wherein the tissue is a frozen section.

29. The method of claim 24, wherein the quantification of the presence or progression of the breast cancer is accomplished by FACS-scan analysis.

30. The method of claim 24, wherein the olignucleotide targets the breast cancer marker survivin.

31. The method of claim 30, wherein the oligonucleotide is one or more selected from the group consisting of SEQ ID NOS: 1, 2 and 9.

32. The method of claim 24, wherein the oligonucleotide targets the breast cancer marker cyclin D1.

33. The method of claim 32, wherein the oligonucleotide is one or more selected from the group consisting of SEQ ID NOS: 3 and 4.

34. The method of claim 24, wherein the oligonucleotide targets the breast cancer marker Her2/neu.

35. The method of claim 34, wherein the oligonucleotide is one or more selected from the group consisting of SEQ ID NOS: 5 and 6.

36. A method of detecting or monitoring presence or progression of pancreatic cancer in a subject comprising:

i) providing a sample of cells from said subject for analysis;

ii) treating the sample with an oligonucleotide that targets a pancreatic cancer marker gene sequence, wherein the oligonucleotide comprises at least one linked energy donor moiety and at least one linked energy acceptor moiety, wherein said oligonucleotide forms a stem-loop hairpin and wherein said donor and acceptor moieties are separated by at least a portion of a probing nucleobase sequence;

iii) detecting, identifying or quantitating the hybridization of the target oligonucleotide sequence to the pancreatic cancer marker gene sequence under suitable hybridization conditions, wherein the presence, absence or amount of

target oligonucleotide sequence present in the sample is correlated with a change in detectable signal associated with at least one donor or acceptor moiety of the oligonucleotide; and

iv) detecting, identifying or quantitating the presence or progression of pancreatic cancer based upon the presence, absence or amount of the hybridization of the oligonucleotide to the breast cancer target sequence that is determined.

37. The method of claim 36, wherein the pancreatic cancer marker is one or more of the markers selected from the group consisting of survivin, a mutant K-*ras* gene, and carcinoembryonic antigen.

38. The method of claim 36, wherein the sample is taken from at least one source selected from the group consisting of blood, urine, pancreatic juice, ascites, needle biopsy or tissue.

39. The method of claim 38, wherein the tissue is a frozen section.

40. The method of claim 36, wherein the quantification of the presence or progression of the pancreatic cancer is accomplished by FACS-scan analysis.

41. The method of claim 36, wherein the olignucleotide targets the pancreatic cancer marker survivin.

42. The method of claim 41, wherein the oligonucleotide is one or more selected from the group consisting of SEQ ID NOS: 1, 2 and 9.

43. The method of claim 36, wherein the oligonucleotide targets a mutant K-*ras* pancreatic cancer marker.

44. The method of claim 43, wherein the oligonucleotide is one or more selected from the group consisting of SEQ ID NOS: 7, 8, 11, 12 and 13.

45. A method of detecting cancerous cells in a sample comprising:

i) providing a sample of cells for analysis;

ii) treating the sample with an oligonucleotide that targets a cancer-specific marker gene sequence, wherein the oligonucleotide comprises at least one linked energy donor moiety and at least one linked energy acceptor moiety,

wherein said oligonucleotide forms a stem-loop hairpin and wherein said donor and acceptor moieties are separated by at least a portion of a probing nucleobase sequence;

iii) detecting, identifying or quantitating the hybridization of the target oligonucleotide sequence to the pancreatic cancer marker gene sequence under suitable hybridization conditions, wherein the presence, absence or amount of target oligonucleotide sequence present in the sample is correlated with a change in detectable signal associated with at least one donor or acceptor moiety of the oligonucleotide; and

iv) detecting, identifying or quantitating the presence cancerous cells based upon the presence, absence or amount of the hybridization of the oligonucleotide to the cancer-specific target sequence that is determined.

46. The method of claim 45, wherein the quantification of the presence of a cancer cell is accomplished by FACS-scan analysis.

47. The method of claim 45, wherein the cancer cell originates from one or more of the cancers selected from the group consisting of: breast, pancreas, ovarian, prostate, colorectal, hepatocellular, multiple myeloma, lymphoma, bladder, medullary carcinoma of the thyroid, neuroendocrine tumors, carcinoid tumors, testicular, gestational trophoblast neoplasms, lung, melanoma and stomach.

48. A diagnostic kit for detecting or monitoring the progession of cancerous cells comprising materials suitable for carrying out the method of claim 36.

49. A diagnostic kit for detecting alterations in gene expression in viable cells in real-time comprising materials suitable for carrying out the method of claim 22.